

FT	Modified_site	87	/note- "carboxymethylated to prevent dimerisation by inter or intra disulphide bridges"
FT	FT	104	/note- "carboxymethylated to prevent dimerisation by inter or intra disulphide bridges"
FT	Peptide	9 ..217	/note- "human Troponin I"
FT	Peptide	9 ..161	/note- "CN-Br cleavage fragment"
FT	Peptide	8 ..219	/note- "CN-Br cleavage fragment"
FT	Peptide	2 ..4	/note- "CN-Br cleavage fragment"
FT	Peptide	5 ..8	/note- "CN-Br cleavage fragment"
FT	Peptide	163 ..208	/note- "CN-Br cleavage fragment"
FT	Peptide	209 ..19	/note- "CN-Br cleavage fragment"
FT	Peptide	220 ..226	/note- "CN-Br cleavage fragment"
FT	Peptide	14 ..101	/note- "CN-Br cleavage fragment"
FT	PN	W09719955-71.	
PD		05-JUN-1997.	
PF		26-NOV-1996; U18878	
PR		29-NOV-1995; US-564526.	
PA		(DADE-) DADE INT INC.	
PT		Demarco C, Moriana NA;	
PT		WPI: 97-310526/8.	
DR		Human cardiac Troponin I cyanogen bromide cleaved fragment - used in calibrator or control for troponin I immunoassay Disclosure; Page 20; 52pp; English.	
PS		The present sequence represents a recombinant form of the cardiac isotype of the myofibrillar contractile protein Troponin I (cTnI). Troponin I is the inhibitory subunit of troponin, a thin filament regulatory protein complex which confers calcium sensitivity to the cardiac and striated muscle. cTnI was cleaved with cyanogen bromide, which cleaves at Met residues with a high specificity under acidic conditions, to generate several fragments. A 153 amino acid CNBr-cTnI isoform is used in a calibrator or a control for a TnI immunoassay. The CNBr-cTnI isoform is comparable in molecular weight to a major degradation product of native cTnI in the serum of patients who have experienced myocardial infarction. The peptide has immunological activity to antibodies against TnI. The CNBr-cTnI isoform has an average of 3-times more reactivity than rTnI and lower non-specific binding, as measured by radial partition immunoassay. It also has increased stability over the synthetic peptide currently used in the Dade TnI immunoassay Sequence 226 AA;	
CC	Query Match	99.7%	Score 680; DB 26; Length 226;
CC	Best Local Similarity	99.0%	Pred. No. 1.12e-54;
CC	Matches	98	1; Mismatches 0; Indels 0; Gaps
CC	Db	8 madgssdaareprpapapirrrssnyrayatephakkskisarsrkqlktllqiaqke 67	
CC	Qy	1 MADGSSDAAREPRPAPAPIRRSSNYRAYATEPHAKKSKISARSRKQLKTLLQIAQKE 60	
CC	Db	68 lereaeerrgkgriastricopelelgfaelqdldrq 106	
CC	Qy	61 LEREAEERRGEKGRIALSTRCOPLELAGLGFAELQDLCRQ 99	
SQ	RESULT	5	standard; Protein: 319 AA.
SQ	ID	W41572	
SQ	AC	W41572;	
SQ	DT	22-JUN-1998 (first entry)	
SQ	DE	Human cardiac troponin I; parvalbumin fusion protein.	
SQ	KW	troponin I; parvalbumin; immunoassay; assay; analysis; human; cardiac muscle; skeletal muscle; injury; myocardial infarction; diagnosis; cTnI; card. Chimeric Homo sapiens.	

DR WPI: 98-062676/06.
 DR N-PSDB: V04225.
 PT Immunoassay of mammalian troponin using stable standard for comparison - specifically acid-dialysed solution or its lyophilisate used for diagnosis of cardiac or skeletal muscle damage
 PT Example 3; Page 67-68; 94PP; English.
 PS This protein sequence comprises a fusion protein with the N-terminal region being human cardiac troponin I (HcTnI) and the C-terminal region being human cardiac troponin C (HcTnC). It has been expressed in E. coli host cells utilising a vector carrying a HcTnI-HcTnC polynucleotide (see V04225) obtained by PCR. The addition of the calcium binding protein HcTnC to HcTnI provided more favourable solubility properties to HcTnI. The invention provides an assay for measuring mammalian, preferably human, troponin in a patient sample. The assay includes the step of comparing the level in the sample with a novel troponin protein standard. This may be a storage stable, soluble mammalian troponin, a functional fragment of the troponin, a modified troponin or its functional fragment, a troponin fusion protein or a heteromultimeric troponin complex (see also W41570-75). The method is used to monitor changes in the level of human troponin, particularly for diagnosis of diseases involving damage to heart or skeletal muscle, e.g. acute myocardial infarction. It may also be used to study normal and pathological functions of troponin-expressing tissues.

SQ Sequence 372 AA;

Query Match 99.4%; Score 678; DB 29; Length 372;
 Best Local Similarity 99.0%; Pred. No. 1.75e-54;
 Matches 98; Conservative 0; Gaps 0;
 Indels 0; Mismatches 1;

Db 1 mgdgssdaareprpapirrrsnnyrayatephakkkksasasklqklqlqkqe 60
 Qy 1 MADGSSDAAREPRPAPIRRRSNNYRAYATEPHAKKKSKISASRKLQLKTLQIAQE 60

Db 61 lereaeerrgekgralstrcpolelaglfqaelqcrq 99
 Qy 61 LEREAERRGEKGRLSTRCPOLELAGLFQELQDCRQ 99

RESULT 7
 ID W18053 standard; protein; 153 AA.
 AC W18053; 7
 DT 20-FEB-1998 (first entry)
 DE Recombinant myofibrillar contractile protein Troponin I CN-Br fragment.
 KW Cardiac isotype; myofibrillar contractile protein; Troponin I; cTnI;
 KW inhibitory subunit; thin filament regulatory protein; TnI immunoassay;
 KW calcium sensitivity; cardiac muscle; striated muscle;
 KW degradation product; cyanogen bromide cleavage; myocardial infarction;
 KW immunological activity.
 OS Homo sapiens.
 PH Location/Qualifiers
 FT Modified_site 79 /note= "carboxymethylated to prevent dimerisation by inter or intra disulphide bridges"
 FT Modified_site 96 /note= "carboxymethylated to prevent dimerisation by inter or intra disulphide bridges"
 PN W0971955-A1.
 PD 05-JUN-1997.
 PF 26-NOV-1995; US-164526.
 PR (DADE) DADE INT INC.
 PA Demarco C, Moriana NA;
 DR 9-310526-2B.

PT Human cardiac Troponin I cyanogen bromide cleaved fragment - used in calibrator or control for troponin I immunoassay
 PT Disclosure; Page 20; 52PP; English.
 PS The present sequence represents a CN-Br cleavage fragment of the recombinant cardiac isotype of the myofibrillar contractile protein cTnI (cTnI). Troponin I is the inhibitory subunit of Troponin, a thin filament regulatory protein complex which confers calcium sensitivity to the cardiac and striated muscle. The present 153 amino

CC acid CNBr-cTnI isoform is used in a calibrator or a control for a TnI immunoassay. The CNBr-cTnI isoform is comparable in molecular weight to a major degradation product of native cTnI in the serum of patients who have experienced myocardial infarction. The Peptide has immunological activity to antibodies against TnI. The CNBr-cTnI isoform has an average of 3-4 times more reactivity than rTnI and lower non-specific binding, as measured by radial partition immunoassay. It also has increased stability over the synthetic peptide currently used in the Dade TnI immunoassay.
 CC Sequence 153 AA;

Query Match 98.1%; Score 669; DB 26; Length 153;
 Best Local Similarity 99.0%; Pred. No. 1.34e-53;
 Matches 97; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 adgssdaareprpapirrrsnnyrayatephakkkksasasklqklqlqkqe 60
 Qy 2 ADGSSDAAREPRPAPIRRRSNNYRAYATEPHAKKKSKISASRKLQLKTLQIAQE 61

Db 61 ereaeerrgekgralstrcpolelaglfqaelqcrq 98
 Qy 62 EREAEERRGEKGRLSTRCPOLELAGLFQELQDCRQ 99

RESULT 8
 ID W02286 standard; peptide; 80 AA.
 AC W02286;
 DT 27-MAY-1997 (first entry)
 DE Human troponin I fragment, residues 2-81 (initial Met is residue 1).
 KW Cardiac heart; troponin I; fragment; analyte; aqueous calibrator;
 KW stabiliser; myosin; myoglobin; lactate dehydrogenase; creatine kinase;
 KW myocardial infarction; heart attack.
 OS Homo sapiens.
 PN W09627561-A1.
 PD 12-SEP-1996.
 PR 06-MAR-1996; US03034.
 PA 07-MAR-1995; US-000158.
 PI Bauer R, Chin B, Flaa C, Sabucedo A;
 DR WPI: 96-425423/42.
 PT Ag. compsn. for stabilising proteins for use as controls for cardiac markers - comprising buffer, reducing agent, stabilising protein,
 PT cheatin agent and salt.
 PS Claim 6; Page 41; 57PP; English.
 CC W02286 and W02286 are troponin I fragments used to exemplify the usefulness of an aqueous composition (may be lyophilised) used as an aqueous calibrator and control solution for diagnostic assays for cardiac proteins and peptides. The stabilising solution comprises a buffer, a reducing agent (e.g. 2-mercaptopropanol or N-acetyl-cysteine), a stabilising protein (e.g. albumin or casein), a chelating agent (e.g. EDTA or EGTA), a salt (e.g. NaCl), a blocking agent (especially gelatine) and a bulking agent (e.g. trehalose, glucose, sucrose, galactose, etc.).
 CC The composition is especially useful for diagnostic assays of troponin, myoglobin, creatine kinase (CK), CK isoenzymes, lactate dehydrogenase (LD), LD isoenzymes, myosin and fragments of these. The composition may be used, e.g. in tests for acute myocardial infarction. The stabilising composition is not derived from human serum, and thus prevents exposure of the user (and manufacturing personnel) to many of the diseases which can be spread by contact with human blood products.
 CC The composition is also able to keep analytes stable in liquid form for extended periods of time.
 CC Sequence 80 AA;

Query Match 78.6%; Score 536; DB 21; Length 80;
 Best Local Similarity 100.0%; Pred. No. 1.28e-40;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 adgssdaareprpapirrrsnnyrayatephakkkksasasklqklqlqkqe 60
 Qy 2 ADGSSDAAREPRPAPIRRRSNNYRAYATEPHAKKKSKISASRKLQLKTLQIAQE 61

Db 61 ereaeerrgekgralstrcq 80
 Qy 62 EREAEERRGEKGRLSTRCQ 81

CC chromatography in the presence of the extraction buffer and calcium ions
 CC thereby to absorb the troponin I. The troponin I is then desorbed by
 CC washing with the aqueous extraction buffer containing EGTA. The protease
 CC inhibitor mixture used comprises at least two cathepsin protease
 CC inhibitors, at least one serine protease inhibitor and at least one
 CC cysteine protease inhibitor. The inhibitor mixture may also contain an
 CC aspartate protease inhibitor, an aminopeptidase protease inhibitor and
 CC a metalloendopeptidase inhibitor. The isolated troponin I can be used as
 CC a standard in detection assays for early detection of myocardial
 CC infarction. The method provides pure and stable troponin which can
 CC provide for reproducible and reliable clinical testing.

Seq	Sequence	31 AA;	Score	202;	DB	21;	Length	31;
	Query Match	29 6%;	Pred. No.	4.88e-09;				
	Best Local Matches	Similarity 100 %;	Mismatches	0;	Indels	0;	Caps	0;
		Matches 31; Conservative						
Db	1	adgsdaareprpapirrrssnyravate	31					
Qy	2	ADGSSDAAREPRPAPIRRRSSNYRAVATE	32					
RESULT	14							
ID	R73032	standard; peptide:	31 AA.					
AC	R73032;							
DT	14-DEC-1995	(first entry)						
DB	N-terminal sequence of cardiac troponin I.							
KW	Cardiac troponin I; ctnI; N-terminal region; cardiac specific; protease inhibitor; myocardial infarction.							
OS	Homo sapiens.							

PN	CA2130280-A.
PD	25-FEB-1995.
PR	17-AUG-1994; 130280.
PR	24-AUG-1993; US-110824.
PA	(SPEC-) SPECTRAL DIAGNOSTICS INC.
PI	Jackowski G, Lee L;
WPI	95-15557/21.
DR	New intact cardiac troponin I from heart tissue - isolated in presence of urea and protease inhibitors, useful as calibrator and quality control standard for troponin assay.
PT	The sequence shown is the N-terminal sequence of cardiac troponin I (cTnI). This sequence was used in the development of a method for purifying cardiac troponin I with increased stability. The method was purify the cTnI in the presence of a mixture of protease inhibitors. This mixture of protease inhibitors includes at least 2 cathepsin protease inhibitors, at least 1 serine protease inhibitor and at least 1 cysteine protease inhibitor. This mixture is effective to inhibit degradation of the cardiac specific N-terminal region of cTnI, which is this sequence. The advantage of this method is that it enables practically intact cTnI that has good storage stability to be isolated. The cTnI may then be used as a sensitive early indicator of myocardial infarction.
CC	Sequence 31 AA;
SQ	1 adgssdaarprapapirrrssnyrayate 31 2 ADGSSDAAREPRAPAPIRRRSSNYRAYATE 32
Query Match	29.68;
Best Local Similarity	100.0%
Matches	31; Conservative
Db	1 adgssdaarprapapirrrssnyrayate 31 2 ADGSSDAAREPRAPAPIRRRSSNYRAYATE 32
Qy	
RESULT	15
ID	W22598 standard; protein: 182 AA.
AC	W22598.
DT	23-MAR-1998 (first entry)
DE	Human fast twitch skeletal muscle troponin I; angiogenesis; inhibitor;
KW	humour; fast twitch skeletal muscle troponin I; angiogenesis; inhibitor;
KW	tumour; ocular neovascularisation; arthritis; psoriasis;
KW	atherosclerotic plaque; nonunion fracture.
OS	Homo sapiens.
PN	WO9730085 A1.
PD	21-AUG-1997.
PR	14-FEB-1997; U02439.
PR	16-FEB-1996; US-602941.
PA	(CHIL-) CHILDRENS MEDICAL CENT.
PI	Langer RS, Moses MA, Szytowski A, Wiederschain DG,
PI	Wu I;
DR	WPI: 97-42497/39.
PT	Use of troponin subunits as angiogenesis inhibitors - used for treating e.g. tumours, ocular neovascularisation, arthritis, psoriasis, atherosclerotic plaques or nonunion fractures
PS	Claim 1; Page 9, 51PP; English.
CC	A novel pharmaceutical composition has been developed which comprises a carrier and an angiogenesis inhibiting amount of a peptide which is:
CC	(a) an inhibitor of basic fibroblast growth factor (bFGF)-stimulated
CC	bovine endothelial cell proliferation having an IC50 of at least 10 mu M; (b) greater than 75 amino acids in length; and (c) greater
CC	than 80% homologous with a Subunit selected from human fast-twitch
CC	troponin subunit C, subunit I or subunit T. The present sequence
CC	represents human fast-twitch troponin subunit I. The compositions can
CC	be used for inhibiting atopic angiogenesis. They can be used to treat a
CC	cancerous condition, or to prevent progression from a pre-neoplastic or
CC	non-malignant state into a neoplastic or a malignant state. They can
CC	also be used to treat ocular disorders associated with
CC	neovascularisation such as neovascular glaucoma, diabetic retinopathy,
CC	retinoblastoma, retrolental fibroplasia, uveitis, retinopathy of
CC	prematurity, macular degeneration, corneal graft neovascularisation as well as other eye inflammatory diseases, ocular tumour and diseases
CC	associated with choroidal or iris neovascularisation. They can also be used to treat other disorders e.g. haemangioma, arthritis, psoriasis,

CC angiofibroma, atherosclerotic plaques, delayed wound healing,
CC granulations, haemophilic joints, hypertrophic scars, nonunion
CC fractures, Osler-Weber syndrome, pyogenic granuloma, scleroderma,
CC trachoma, and vascular adhesions.
SQ Sequence
182 AA;

Query Match 29.5%; Score 201; DB 26; Length 182;
Best Local Similarity 39.7%; Pred. No. 5.99e-09;
Matches 25; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
Db 6 krrraitarrqhlksvmlqiaatelekesrekekqnylaehcpplhipg-smsevgel 64
|:|::|:||:|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
37 KKSKitASRNLQLKTLQTLQTAKEERGEKRALSTRCOPELAGLFAELQDL 96
QY
65 ckg 67
|:|:
97 CRQ 99

Search completed: Fri Jan 21 14:31:17 2000
Job time : 60 secs.

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#map_position 19p13.2-19q13.2
COMPLEX troponin I, a heterotrimer with one molecule each of troponin C (calcium binding component), troponin I (inhibitory component), and troponin T (tropomyosin-binding component)

FUNCTION binds actin and inhibits myosin ATPase activity; with tropomyosin mediates contraction of vertebrate striated muscle in response to calcium

#pathway

CLASSIFICATION

KEYWORDS

FEATURE

2

23, 24

SUMMARY

Query Match 100.0%; Score 682; DB 1; Length 210;
Best Local Similarity 100%; Pred. No. 1.3e-103; Indels 0; Gaps 0;
Matches 99; Conservative 0; Mismatches 0;

Db 1 MADGSSDAREPRPAPIRRSSNYRAYATEPHAKKSISASRKQLQKTLIQTAKQE 60
QY 1 MADGSSDAREPRPAPIRRSSNYRAYATEPHAKKSISASRKQLQKTLIQTAKQE 60

Db 61 LEREAEEERGEKGRALSTRCOPPLELAGLGFATQDLCRQ 99
Qy 61 LEREAEEERGEKGRALSTRCOPPLELAGLGFATQDLCRQ 99

RESULT

2

A53805 #type complete
troponin I, cardiac - mouse

ORGANISM

DATE 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-1999

ACCESSIONS

REFERENCE

Authors Guo, X.; Wattanapenpoool, J.; Palmiter, K.A.; Murphy, A.M.; Solano, R.J.

Journal J. Biol. Chem. (1994) 269:15210-15216

#title Mutagenesis of cardiac troponin I. Role of the unique NH₂-terminal peptide in myofilament activation.

#cross-references MUID:94253083

#status preliminary

#molecule_type mRNA

#residues 1-211 #label GUO

#cross-references GB:U09181; NID:9484093; PID:9508866

REFERENCE

Authors Ausoni, S.; Campione, M.; Picard, A.; Moretti, P.; Vitadello, M.; De Nardi, C.; Schiaffino, S.

Journal J. Biol. Chem. (1994) 269:339-346

#title Structure and regulation of the mouse cardiac troponin I gene

#cross-references MUID:94103233

#accession A53108

#status preliminary; translated from GB/EMBL/DDJB

#molecule_type DNA

#residues 1-111 #label RES

#cross-references EMBL:Z2274; NID:g313104; PID:g313105

GENETICS

#introns 4/2; 8/3; 37/3; 51/3; 95/3; 125/3; 184/3

CLASSIFICATION

KEYWORDS

SUMMARY

Query Match 100.0%; Score 614; DB 2; Length 211;
Best Local Similarity 89.0%; Pred. No. 8.63e-91; Indels 1; Gaps 1;
Matches 89; Conservative 0; Mismatches 6;

Db 1 MADESSDAGEQPAPVRRSSNYRAYATEPHAKKSISASRKQLQKTLIQTAKQE 60
QY 1 MADGSSDAREPRPAPIRRSS-NYRAYATEPHAKKSISASRKQLQKTLIQTAKQE 59

RESULT

3

A60124 #type complete
troponin I, cardiac muscle - rat

ORGANISM

DATE 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 31-Oct-1997

ACCESSIONS

REFERENCE

Authors Ausoni, S.; De Nardi, C.; Moretti, P.; Gorza, L.; Schiaffino, S.

#journal Development (1991) 112:1041-1051

#title Developmental expression of rat cardiac troponin I mRNA.
#accession A60124

#molecule_type mRNA

#residues 1-211 #label AUS

#cross-references EMBL:X5849; NID:956022; PID:956023

REFERENCE

Authors Murphy, A.M.; Jones II, L.; Sims, H.F.; Strauss, A.W.

Journal Biochemistry (1991) 30:707-712

#title Molecular cloning of rat cardiac troponin I and analysis of troponin I isoform expression in developing rat heart.

#cross-references MUID:9105162

#accession A33398

#molecule_type mRNA

#residues 1-211 #label MUR

#cross-references GB:M51679; NID:9207509; PID:9207510

CLASSIFICATION

KEYWORDS

SUMMARY

Query Match 89.4%; Score 610; DB 2; Length 211;
Best Local Similarity 89.0%; Pred. No. 4.9e-90; Indels 1; Gaps 1;
Matches 89; Conservative 4; Mismatches 6;

Db 1 MADESSDAGEQPAPVRRSSNYRAYATEPHAKKSISASRKQLQKTLIQTAKQE 60
QY 1 MADGSSDAREPRPAPIRRSS-NYRAYATEPHAKKSISASRKQLQKTLIQTAKQE 59

RESULT

4

156441 #type complete
troponin I - rat

ORGANISM

DATE 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Feb-1997

ACCESSIONS

REFERENCE

Authors Martin, A.F.; Orlowski, J.

Journal J. Mol. Cell. Cardiol. (1991) 23:583-588

#title Molecular cloning and developmental expression of the rat cardiac-specific isoform of troponin I.

#cross-references MUID:9135915

#accession 156441

#status preliminary; translated from GB/EMBL/DDJB

#molecule_type mRNA

#residues 1-211 #label RES

#cross-references GB:M9204; NID:9207515; PID:9207516

CLASSIFICATION

KEYWORDS

SUMMARY

Query Match 90.0%; Score 614; DB 2; Length 211;
Best Local Similarity 89.0%; Pred. No. 8.63e-91; Indels 1; Gaps 1;
Matches 89; Conservative 4; Mismatches 6;

Query Match 89.1%; Score 608; DB 2; Length 211;
 Best Local Similarity 88.0%; Pred. No. 1.16e-89; Length 216;
 Matches 88; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

Db 1 MADESSDAGEPQAPAPVRRSSANYRAYATEPHAKKSKIASRKQLQTLMLQIAKQ 60
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Qy 1 MADGSSDAAREPAPAPIRRS-NYRAYATEPHAKKSKIASRKQLQTLMLQIAKQ 59

Db 61 EMEERAERGEKGRALSTRCQPLYLDGJFEELQDLCRQ 100
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Qy 60 ELEREERGEKGRALSTRCQPLLAGLGFAELQDLCRQ 99

RESULT 5 TPRBC #type complete
 ENTRY troponin I, cardiac muscle - rabbit
 ORGANISM #formal_name Oryctolagus cuniculus #common_name domestic
 rabbit
 DATE 24-Apr-1984 #sequence_revision 03-May-1996 #text_change
 A0096; A90296; S12886; A03090
 ACESSIONS A90296
 REFERENCE Grand, R.J.A.; Wilkinson, J.M.
 #authors Biochem. J. (1977) 167:18-192
 #journal The amino acid sequence of rabbit slow-muscle troponin I.
 #title #cross-references MUID:78060292
 #accession A90296
 #molecule_type Protein
 ##residues 1-4,'R',6-16,18-20,22,'D',27-211 #label GRA
 REFERENCE A90294
 #authors Grand, R.J.A.; Wilkinson, J.M.; Mole, L.E.
 #journal Biochem. J. (1976) 159:63-641
 #title The amino acid sequence of rabbit cardiac troponin I.
 #cross-references MUID:77037072
 #accession A90294
 #molecule_type Protein
 ##residues 1-4,'R',6-11,'K',13-16,18-20,22,'D',27-211 #label GR2
 REFERENCE S12886
 #authors Mittmann, K.; Jaquet, K.; Heilmeyer Jr., L.M.G.
 #journal FEBS Lett. (1990) 273:1-45
 #title A common motif of two adjacent phosphoserines in bovine,
 rabbit and human cardiac troponin I.
 #cross-references MUID:91032199
 #accession S12886
 #molecule_type Protein
 ##residues 1-36 #label MIT
 #note peptide sequences corrected; amino terminal acetylation;
 phosphorylation sites

REFERENCE A93181
 #authors Solar, R.J.; Moir, A.J.G.; Perry, S.V.
 #journal Nature (1976) 262:615-617
 #title Phosphorylation of troponin I and the inotropic effect of
 adrenalin in the perfused rabbit heart.
 #cross-references MUID:76267707
 #contents annotation: phosphorylation sites
 troponin I is a heterotrimer with one molecule each of troponin
 C (calcium binding component), troponin I (inhibitory
 component), and troponin T (tropomyosin-binding component)
 FUNCTION binds actin and inhibits myosin ATPase activity with
 tropomyosin mediates contraction of vertebrate striated
 muscle in response to calcium
 #pathway #superfamily troponin I
 #classification acetylated amino end; actin binding; cardiac muscle; heart;
 #KEYWORDS muscle contraction; phosphoprotein
 FEATURE 1 #modified_site acetylated amino end (Ala) #status
 #experimental #binding_site phosphate (Ser) (covalent) (by
 CAMP-dependent kinase) #status experimental
 SUMMARY #length 211 #molecular_weight 6537
 #length 211 #molecular_weight 24067 #checksum 6537

RESULT 6 A29994 #type complete
 ENTRY troponin I, cardiac muscle - bovine
 ORGANISM #formal_name Bos primigenius taurus #common_name cattle
 DATE 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change
 07-Feb-1997
 ACCESSIONS A29994; S02628
 REFERENCE A29994
 #authors Lesyk, J.; Dumawala, R.; Potter, J.D.; Collins, J.H.
 #journal Biochemistry (1988) 27:2821-827
 #title Amino acid sequence of bovine cardiac troponin I.
 #cross-references MUID:88294022
 #accession A29994
 #molecule_type Protein
 ##residues 1-211 #label LES
 REFERENCE S02628
 #authors Swiderlik, K.; Jaquet, K.; Meyer, H.E.; Heilmeyer Jr., L.M.G.
 #journal Eur. J. Biochem. (1988) 176:335-342
 #title Cardiac troponin I, isolated from bovine heart, contains two
 adjacent phosphoserines. A first example of phosphoserine
 determination by derivatization to S-ethylcysteine.
 #accession S02628
 #molecule_type protein
 ##residues 21-27, Y, 28-37 #label SWI
 #note authors comment in a note added in proof that the extra
 tyrosine is an error
 #superfamily troponin I
 #classification acetylated amino end; actin binding; cardiac muscle; heart;
 #KEYWORDS muscle; phosphoprotein
 FEATURE 1 #modified_site acetylated amino end (Ala) #status
 #experimental #binding_site phosphate (Ser) (covalent) #status
 #experimental
 SUMMARY #length 211 #molecular_weight 23922 #checksum 5928
 Query Match 85.9%; Score 586; DB 2; Length 211;
 Best Local Similarity 88.7%; Pred. No. 1.54e-85;
 Matches 86; Conservative 6; Mismatches 3; Indels 2; Gaps 2;

Db 5 GGSTAG-DTVAPPVRRSSANYRAYATEPHAKKSKIASRKQLQTLMLQIAKQEL 63
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Qy 4 GSSDAAREPAPAPIRRS-NYRAYATEPHAKKSKIASRKQLQTLMLQIAKQEL 62
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 64 REAEERRGEKGRALSTRCQPLLAGLGFAELQDLCRQ 100
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Qy 63 REAEERRGEKGRALSTRCQPLLAGLGFAELQDLCRQ 99
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 RESULT 7 A41030 #type complete
 ENTRY troponin I, cardiac muscle - quail
 #formal_name Coturnix coturnix #common_name quail
 #cross-references MUID:30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
 08-Sep-1997
 ACCESSIONS A41030
 #authors Hastings, K.E.M.; Koppe, R.I.; Marmor, E.; Bader, D.;
 Shimada, Y.; Toyota, N.

#journal J. Biol. Chem. (1991) 266:19659-19665
 #title skeletal muscle troponin I mRNAs.
 #mRNA isoforms. cDNA clone analysis of avian cardiac troponin I
 #cross-references MUID:89340548
 #accession A4786
 #molecule_type mRNA
 #residues 1-187 #label HAS
 #cross-references GB:J04933; NID:g207517; PID:g207518
 CLASSIFICATION #superfamily troponin I
 KEYWORDS actin binding; cardiac muscle; heart
 SUMMARY #length 208 #molecular-weight 23601 #checksum 578

Query Match 63.2%; Score 431; DB 2; Length 208;
 Best Local Similarity 67.4%; Pred. No. 7.90e-57;
 Matches 62; Conservative 12; Mismatches 17; Indels 1; Gaps 1;

Db 2 AEEEPKPPLRKSSANTRYGAPEPHAKROSKITASRSRKQLQKTLLORAKRDLEEREQE 61
 Qy 9 AREPRPAPIRRSS-NYRAYATEPHAKKKSKITASRSRKQLQKTLLOIAKOLEEREGKRALSTRCOPPLELAGLGFAE 92

Db 62 RAGEKQRHIGELCPPPELDLGLAQQLCIRE 93
 Qy 68 RRGKGRALSTRCOPPLELAGLGFAELQDLCRQ 99

RESULT 10 TPHUJTW #type complete
 ENTRY troponin I, slow skeletal muscle - human
 TITLE #formal_name Homo sapiens #common_name man
 ORGANISM #sequence_revision 03-May-1996 #text_change
 DATE 06-Jan-1995 #sequence_revision 03-May-1996
 ACCESSIONS A53740
 REFERENCE #authors Corrin, S.J.; Juhasz, O.; Zhu, L.; Conley, P.; Kedes, L.;
 Drysdale, R.; Wade, R.; J. Biol. Chem. (1994) 269:10651-10659
 #journal J. Biol. Chem.
 #title Structure and expression of the human slow twitch skeletal
 muscle troponin I gene.
 #cross-references MUID:94193765
 #accession A53740
 #molecule_type DNA
 #residues 1-187 #label COR
 REFERENCE A35355
 #cross-references GB:L21905
 #authors Wade, R.; Eddy, R.; Shows, T.B.; Kedes, L.
 #journal Genomics (1990) 7:346-357
 #title cDNA sequence, tissue-specific expression, and chromosomal
 mapping of the human slow-twitch skeletal muscle isoform of
 troponin I
 #cross-references MUID:90307007
 #accession A35355
 #molecule_type mRNA
 #residues 1-181 #label WAD
 #cross-references GB:J04760; NID:9339964; PID:9339965
 GENETICS
 #gene CDB:TNNI1
 #map_position 1q22-1q22
 #intons 4/2; 5/3; 19/3; 63/3; 93/3; 152/3
 #note the first intron occurs before the initiator codon
 troponin I is a heterotrimer with one molecule each of troponin
 C (calcium binding component), troponin I (inhibitory
 component), and troponin T (tropomyosin-binding component)

FUNCTION binds actin and inhibits myosin ATPase activity; with
 troponin I, slow skeletal muscle - rat
 #description troponin I mediates contraction of vertebrate striated
 muscle in response to calcium
 #pathway muscle contraction
 #superfamily troponin I
 #calcium binding component
 #inhibitory component
 #actin binding component
 #troponin T (tropomyosin-binding component)

RESULT 9 B44786 #type complete
 ENTRY troponin I, slow skeletal muscle - rat
 #cross-references GB:J04933; NID:g207517; PID:g207518
 #organism Rattus norvegicus #common_name Norway rat
 #date 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change
 #modified_site acetylated amino end (PRO) (in mature
 form) #status predicted

Db 25 VAPEPPKPAPPAPAPPAPPLIRRSSANVRSYATEQVKRPKTSASKLQLNTMLOIKA 84
 Qy 1 MADGSSDAAREPAPAPPIRRISS-NYRAYATEPHAKKKSKITASRSRKQLKTLLOIKAQK 59

Db 85 ENEREEERDERRKERYIAEHCPOLQSLGSRELQDICE 124
 Qy 60 ELEREAEERGEKGRALSTRCOPPLELAGLGFAELQDLCRQ 99

RESULT 9 B44786 #type complete
 ENTRY troponin I, slow skeletal muscle - rat
 #cross-references GB:J04933; NID:g207517; PID:g207518
 #organism Rattus norvegicus #common_name Norway rat
 #date 17-Mar-1999 #sequence_revision 17-Mar-1999 #text_change
 #modified_site acetylated amino end (PRO) (in mature
 form) #status predicted

ACCESSIONS A44786
 REFERENCE Koppe, R.I.; Hallauer, P.L.; Karpati, G.; Hastings, K.E.M.
 #authors J. Biol. Chem. (1989) 264:14227-14333
 #journal CDNA clone and expression analysis of rodent fast and slow


```

##cross-references GB:L04347
##experimental_source skeletal muscle
##note sequence extracted from NCBI backbone (NCBIP:120236) and
corrected to correspond with the published sequence
##note the authors translated the codons GGC for residue 56 as
Gln, and TAT for residue 80 as Thr

REFERENCE A93193
  #authors Wilkinson, J.M.; Grand, R.J.A.
  #journal Nature (1979) 21:31-35
  #title Comparison of amino acid sequence of troponin I from
different striated muscles.

#cross-references MVID:78114026
#accession A93193
#molecule_type protein
#residues 2-154,158-182 #label WIL

REFERENCE A902886
  #authors Wilkinson, J.M.; Grand, R.J.A.
  #journal Biochem. J. (1975) 149:493-496
  #title The amino acid sequence of troponin I from rabbit skeletal
muscle.

#cross-references MVID:76039510
#accession A902886
#molecule_type protein
#residues 2-114,'R',115-154,158-182 #label WI2

REFERENCE A91408
  #authors Moir, A.J.G.; Wilkinson, J.M.; Perry, S.V.
  #journal FEBS Lett. (1974) 42:253-256
  #title The phosphorylation sites of troponin I from white skeletal
muscle of the rabbit.

#cross-references MVID:74309023
#contents annotation; phosphorylation sites
A91407
  #authors Huang, T.S.; Bylund, D.B.; Stull, J.T.; Krebs, E.G.
  #journal FEBS Lett. (1974) 42:249-252
  #title The amino acid sequences of the phosphorylated sites in
troponin I from rabbit skeletal muscle.

#cross-references MVID:74308154
#contents annotation; phosphorylation sites
I46471
  #authors Putney, S.D.; Herlihy, W.C.; Schimmel, P.
  #journal Nature (1983) 302:718-721
  #title A new troponin T and cDNA clones for 13 different muscle
proteins found by shotgun sequencing.

#cross-references MVID:83167564
#accession I46514
  #status preliminary; translated from GB/EMBL/DDJB
#molecule_type mRNA
#residues 166-178 #label PUT

##cross-references EMBL:V03898; NID:91738; PID:9929767
COMPLEX troponin is a heterotrimer with one molecule each of troponin
C (calcium binding component), troponin I (inhibitory
component), and troponin T (tropomyosin-binding component)

FUNCTION binds actin and inhibits myosin ATPase activity; with
tropomyosin mediates contraction of vertebrate striated
muscle in response to calcium
#description #superfamily troponin I
#pathway #modified-site acetylated amino end (Gly) (in mature
form) #status experimental\

FEATURE 2
  #binding_site phosphate ('Thr') (covalent) (by
  #CAMP-dependent kinase) #status experimental\
  #binding-site phosphate ('Ser') (covalent) (by
  #CAMP-dependent kinase) #status experimental

SUMMARY #length 182 #molecular-weight 21214 #checksum 8861
  Query Match 30.8%; Score 208; DB 1; Length 182;
  Best Local Similarity 42.9%; Pred. No. 1;12e-17; Indels 1; Gaps 1;
  Matches 27; Conservative 19; Mismatches 16; Del 1; CQ 99

Search completed: Fri Jan 21 14:29:58 2000
Job time : 29 secs.

Db 6 KRNRAITAROHLKSYMLOQIAATELEKEEERAEKQNYLAERCPPLSLEG-SMAEVQEL 64
Qy 37 KKSISASRKQLQLTLLQIAKQELEREERERSEKGRALSTRCQPLEAGLGFAELQDL 96
Db 65 CKQ 67
Qy 97 CQ 99

RESULT 15 A44786 #type complete
ENTRY troponin I fast skeletal muscle - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change
17-Mar-1999

ACCESSIONS A44786
REFERENCE Koppe, R.I.; Hallauer, P.L.; Karpatti, G.; Hastings, K.E.M.
#authors #journal #title
#cross-references GB:J01992; NID:9202164; PID:g202165
CLASSIFICATION #superfamily troponin I
KEYWORDS skeletal muscle #molecular-weight 21357 #checksum 306
#length 182

#CROSS-references MUID:8930548
#accession A44786
#status preliminary
#molecule_type mRNA
#residues 1-182 #label KOP
#cross-references GB:J01992; NID:9202164; PID:g202165
#superfamily troponin I
#length 182

Query Match 30.18; Score 205; DB 2; Length 182;
Best Local Similarity 41.3%; Pred. No. 3.49e-17;
Matches 26; Conservative 20; Mismatches 16; Indels 1; Gaps 1;
Db 6 KRNRAITAROHLKSYMLOQIAATELEKEEERAEKQNYLAERCPPLHIPS-SMSEVQEL 64
Qy 37 KKSISASRKQLQLTLLQIAKQELEREERERSEKGRALSTRCQPLEAGLGFAELQDL 96
Db 65 CKQ 67
Qy 97 CQ 99

Search completed: Fri Jan 21 14:29:58 2000
Job time : 29 secs.

Db 6 KRNRAITAROHLKSYMLOQIAATELEKEEERAEKQNYLAERCPPLSLEG-SMAEVQEL 64
Qy 37 KKSISASRKQLQLTLLQIAKQELEREERERSEKGRALSTRCQPLEAGLGFAELQDL 96
Db 65 CKQ 67
Qy 97 CQ 99

```


QY 8 AAREPRPAPAPIRRSSNYRAYATEPHAKK-KSKSISAS-RKQLQTKLIL-QLI-AKQELER 63
 DB 570 QPP-PR-EPARAOAPN-HRVQGLGLGTAPLNG 598
 QY 64 EAERRGEKGRLSTRCOPLEAGLGFAELQD 95

RESULT 12
 ID O44077 PRELIMINARY; PRT; 271 AA.
 AC :|||: ;:::|||: ;:::|||:
 DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DE TROPONIN I (FRAGMENT).
 OS CHIAMY'S NIPPONENSIS AKAZARA (AKAZARA SCALLOP) (JAPANESE SCALLOP).
 OC EUKARYOTA; METAZOA; MOLLUSCA; BIVALVIA; PTERIOMORPHIA; OSTREOIDA;
 OC PECTINIDAE; CHLAMYDAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA NISHITA K., OJIMA T., SOEIJIMA T.;
 SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
 DR AB009368; D1024380; -.
 SQ SEQUENCE 271 AA; 32068 MW; C9E22FB9 CRC32;

Query Match Score 104; DB 5; Length 293;
 Best Local Similarity 28.8%; Pred. No. 2.18e-02;
 Matches 17; Conservative 14; Mismatches 28; Indels 0; Gaps 0;

RA Hotta A.L.;
 DR SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
 DR EMBL; AB009305; D1024722; -.
 DR PFAM; PF00932; Tropomin; 1.
 SQ SEQUENCE 314 AA; 37009 MW; EB5A2098 CRC32;

Query Match Score 15.2%; Score 104; DB 5; Length 293;
 Best Local Similarity 28.8%; Pred. No. 2.18e-02;
 Matches 17; Conservative 14; Mismatches 28; Indels 0; Gaps 0;

RA Hotta A.L.;
 DR SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
 DR EMBL; AB009305; D1024722; -.
 DR PFAM; PF00932; Tropomin; 1.
 SQ SEQUENCE 314 AA; 37009 MW; EB5A2098 CRC32;

Query Match Score 15.2%; Score 104; DB 5; Length 314;
 Best Local Similarity 28.8%; Pred. No. 2.18e-02;
 Matches 17; Conservative 14; Mismatches 28; Indels 0; Gaps 0;

RA Hotta A.L.;
 DR SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
 DR EMBL; AB009305; D1024722; -.
 DR PFAM; PF00932; Tropomin; 1.
 SQ SEQUENCE 314 AA; 37009 MW; EB5A2098 CRC32;

RESULT 15
 ID Q23585 PRELIMINARY; PRT; 306 AA.
 AC Q23585;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE SIMILAR TO TROPONIN I. NCBI GI: 1072235.
 GN ZK71-2.
 OS CAENORHABDITIS ELEGANS.
 OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTIA; RHABDITIDA;
 OC RHABDITINA; RHABDITOIDEA; RHABDITIDA; PELODERINAE; CAENORHABDITIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94150718.

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., COULSON A.,
 RA BONEFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., FULTON L.,
 RA CRAXTON M., DEAR S., DU S., DURBIN R., FAVELL A., FUJITA M.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MC MURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALLON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MLEG J., THOMAS K., VAUDIN M., VAUGIRAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON S., WILDMAN P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL NATURE 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MILLER N.;
 RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA WATERSTON R.;
 DR SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
 DR EMBL; U40931; G1072235; -.
 DR PFAM; PF00932; Tropomin; 1.
 SQ SEQUENCE 306 AA; 35183 MW; C284B70F CRC32;

Query Match Score 14.8%; Score 101; DB 5; Length 306;
 Best Local Similarity 23.8%; Pred. No. 5.65e-02;
 Matches 20; Conservative 25; Mismatches 37; Indels 2; Gaps 2;

DB 145 ISPEKKKMLKLMQKAEDLNAAKAKAEKYINDLVPKFSTDGKDVAALQALCKD 181
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DE TROPONIN I.
 OS PATINOPECTEN YESSOENSIS (EZO GIANT SCALLOP) (YESSO SCALLOP).
 OC EUKARYOTA; METAZOA; MOLLUSCA; BIVALVIA; PTERIOMORPHIA; OSTREOIDA;
 OC PECTINIDAE; PATINOPECTEN.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hotta A.L.;
 RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
 DR EMBL; AB00806; D1023723; -.
 DR PFAM; PF00932; Tropomin; 1.
 SQ SEQUENCE 293 AA; 34670 MW; 49299FDE CRC32;

Query Match Score 15.2%; Score 104; DB 5; Length 293;
 Best Local Similarity 28.8%; Pred. No. 2.18e-02;
 Matches 17; Conservative 14; Mismatches 28; Indels 0; Gaps 0;

DB 145 ISPEKKKMLKLMQKAEDLNAAKAKAEKYINDLVPKFSTDGKDVAALQALCKD 203
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DE TROPONIN I.
 OS PATINOPECTEN YESSOENSIS (EZO GIANT SCALLOP) (YESSO SCALLOP).
 OC PECTINIDAE; PATINOPECTEN.
 RN [1]
 RP SEQUENCE FROM N.A.

RESULT 14
 ID O15987 PRELIMINARY; PRT; 314 AA.
 AC O15987;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DE TROPONIN I.
 OS EUKARYOTA; METAZOA; MOLLUSCA; BIVALVIA; PTERIOMORPHIA; OSTREOIDA;
 OC PECTINIDAE; PATINOPECTEN.
 RN [1]
 RP SEQUENCE FROM N.A.

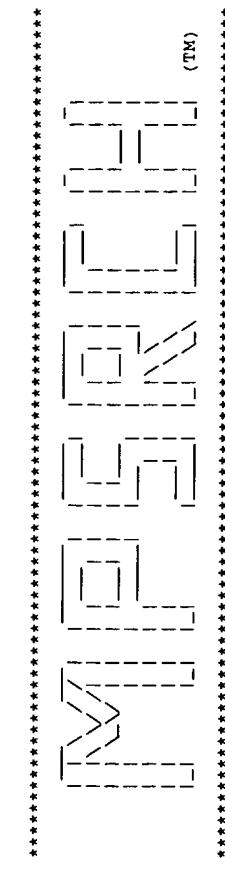
DB 124 DLKQOLKLQEQRQKALADRTISL 147
 AC :|||: ;:::|||: ;:::|||:
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DE TROPONIN I.
 OS EUKARYOTA; METAZOA; MOLLUSCA; BIVALVIA; PTERIOMORPHIA; OSTREOIDA;
 OC PECTINIDAE; PATINOPECTEN.
 RN [1]
 RP SEQUENCE FROM N.A.

QY 60 ELEREAERGERGEKGRLSTRCQPL 83

QY 1 MADGSSDAAREPRPAPAPIRRSSSNYRAYATEPHAK-KRSKISASRKQLKLLQIARK 59

QY 124 DLKQOLKLQEQRQKALADRTISL 147
 AC :|||: ;:::|||: ;:::|||:
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DE TROPONIN I.
 OS EUKARYOTA; METAZOA; MOLLUSCA; BIVALVIA; PTERIOMORPHIA; OSTREOIDA;
 OC PECTINIDAE; PATINOPECTEN.
 RN [1]
 RP SEQUENCE FROM N.A.

Search completed: Fri Jan 21 14:29:12 2000
 Job time : 52 secs.



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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Jan 21 14:27:43 2000; Maspar time 4.57 Seconds
612.656 Million cell updates/sec

Tabular output not generated.

Title: >US-09-176-546-2
Description: (1-99) from US09176546 . pep
Perfect Score: 682
Sequence: 1 MADGSSDAAREPRPAPIR.....CQPLELAGLGFAELQDLCRQ 99

Scoring table: PAM 150
Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
1:swissprot

Statistics: Mean 41.275; Variance 77.899; scale 0.530

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description	Pred. No.
1	671	98.4	209	1 TRIC_HUMAN TROPONIN I, CARDIAC MU	1 63e-116
2	603	88.4	210	1 TRIC_MOUSE TROPONIN I, CARDIAC MU	7.86e-102
3	599	87.8	210	1 TRIC_RAT TROPONIN I, CARDIAC MU	5.70e-101
4	586	85.9	211	1 TRIC_BOVINE TROPONIN I, CARDIAC MU	3.54e-98
5	539	79.0	206	1 TRIC_RABBIT TROPONIN I, CARDIAC MU	4.07e-98
6	431	63.2	207	1 TRIC_COTTON_TROPOONIN_I, CARDIAC MU	2.70e-65
7	429	62.9	243	1 TRIC_XENIA TROPONIN I, CARDIAC MU	7.28e-65
8	268	39.3	168	1 TRIC_CHICK TROPONIN I, CARDIAC MU	4.71e-32
9	237	34.8	186	1 TRIC_RAT TROPONIN I, SLOW SKEL	5.03e-26
10	231	33.9	186	1 TRIC_HUMAN TROPONIN I, SLOW SKEL	7.12e-25
11	219	32.1	184	1 TRIC_RABBIT TROPONIN I, SLOW SKEL	1.36e-22
12	208	30.5	181	1 TRIC_RABBIT TROPONIN I, FAST SKEL	1.60e-20
13	205	30.1	181	1 TRIC_MOUSE TROPONIN I, FAST SKEL	5.81e-20
14	203	29.8	181	1 TRIC_RAT TROPONIN I, FAST SKEL	1.37e-19
15	201	29.5	181	1 TRIC_HUMAN TROPONIN I, FAST SKEL	3.22e-19
16	192	28.2	182	1 TRIC_CHICK TROPONIN I, FAST SKEL	1.48e-17
17	143	21.0	259	1 TRIDROME TROPONIN I (TNI) (WING)	6.49e-09
18	136	19.9	201	1 TRIPONINE TROPONIN I	9.47e-08
19	110	16.1	564	1 EMRI_XENIA FRAGILE_X MENTAL RETAR	1.20e-08
20	103	15.1	648	1 EXRI_XENIA FRAGILE_X MENTAL RETAR	1.28e-02
21	101	14.8	257	1 TRIC_HUMAN TROPONIN T, FAST SKEL	2.49e-02
22	93	13.6	278	1 TRIC_RABBIT TROPONIN T, FAST SKEL	3.24e-01
23	93	13.6	886	1 CHS_SAPMO CHITIN SYNTHASE (EC 2.	3.24e-01

RESULT		ALIGNMENTS	
ID	TRIC_HUMAN	STANDARD:	PRT: 209 AA.
AC	P19423;		
DT	01-FEB-1991 (REL 17, CREATED)		
DT	01-AUG-1992 (REL 23, LAST SEQUENCE UPDATE)		
DT	01-NOV-1997 (REL 35, LAST ANNOTATION UPDATE)		
DE	TROPONIN I, CARDIAC MUSCLE.		
GN	TNNI3 OR TNNC1.		
OS	HOMO SAPIENS (HUMAN)		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=HEART MUSCLE;		
RX	MEDLINE: 91032031.		
RX	VALINS W.J., BRAND N.J., DABHADE N., BUTLER-BROWNE G.,		
RA	"Cloning and expression in Escherichia coli of the cDNA encoding human cardiac troponin I."		
RA	YACOUB M.H., BARTON P.J.R.;		
RT	"Molecular cloning of human cardiac troponin I using polymerase chain reaction."		
RT	FEBS LETT. 270:57-61(1990).		
RL			
RN	[2]		
RP	REVISION TO 85, SEQUENCE FROM N.A.		
RX	MEDLINE: 94010323.		
RA	ARMOUR K.L., HARRIS W.J., TEMPEST P.R.;		
RT	"Cloning and expression in Escherichia coli of the cDNA encoding human cardiac troponin I."		
RT	GENOMICS 35:11-23(1996).		
RL			
RN	[3]		
RP	SEQUENCE FROM N.A.		
RX	HUNKELER N.M., KULLMAN J., MURPHY A.M.;		
RA	"Troponin I isoform expression in human heart."		
RT	RT CIR. RES. 69:1409-1414 (1991).		
RT	"Isolation and characterization of the human cardiac troponin I gene (TN13)."		
RT	RT GENOMICS 35:11-23(1996).		
RL			
RN	[4]		
CC	-!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERs CALCIUM-SENSITIVITY		
CC	-!- TO STRIATED MUSCLE ACTOMYOSIN ATPase ACTIVITY.		
CC	-!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.		
CC	-!- TROPONIN I entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation		
CC	-!- TROPONIN I entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation		

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or send an email to licensing@sci.csi.ac.cn

CC DR EMBL: Z22784; G313105; -;
CC DR EMBL: U00181; G30866; -;
DR MGD: MG1198783; TNNI3;
DR MGD: MG1198784; TNNI3;
DR MGD: MG1198785; TNNI3;

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Query Match	58.5%	Score 58.5%	DB 1;	Leng
Best Local Similarity	88.7%	Pred. No.	3.46e-88	
FTT	CONFLICT	16	16	(IN REF 1,2).
SQ	SEQUENCE	211 AA:	23922 MW:	DAADBEC0 CRC32;

Qy 62 EREAEERGEKGRALSTRCPPELAGLGFAELQDLCRQ 99

RESULT 6 STANDARD; PRT; 207 AA.
 ID TRIC_COTJA
 AC P27672;
 DT 01-AUG-1992 (REL. 23, CREATED)
 DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DS COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
 OC NEognathae; GALLIFORMES; PHASIANIDAE; PHASIANAE; COTURNIX.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX HASTINGS K.E., KOPPE R.I., MARMUR E., BADER D., SHIMADA Y.,
 RA TOURA N.;
 RT "Structure and developmental expression of tropomodulin I isoforms. cDNA
 clone analysis of avian cardiac tropomodulin mRNA.";
 RT J. BIOL. CHEM. 266:19653-19651(1991).
 RC -!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE
 THIN FILAMENT REGULATORY COMPLEX WHICH CONFERs CALCIUM-SENSITIVITY.
 CC TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
 CC -!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
 CC -!- DEVELOPMENTAL STAGE: HEART.
 CC -!- TISSUE SPECIFICITY: HEART.
 CC -!- EXPRESSED AT ALL STAGES OF DEVELOPMENT.

RT expression during abnormal heart morphogenesis.;"

RL DEV. BIOL. 165:432-441(1994).
 CC -!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE
 THIN FILAMENT REGULATORY COMPLEX WHICH CONFERs CALCIUM-SENSITIVITY.
 CC TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
 CC -!- TISSUE SPECIFICITY: HEART.
 CC -!- EXPRESSED AT ALL STAGES OF DEVELOPMENT.

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DR EMBL; L25721; G410051;
 DR PFAM; PF00992; tropomodulin 1.
 KW MUSCLE PROTEIN; ACTIN-BINDING.
 FT INIT_MET 0 BY SIMILARITY.
 FT DOMAIN 9 14 POLY-GLU.
 FT DOMAIN 17 22 POLY-GLU.
 FT DOMAIN 84 91 POLY-GLU.
 SQ SEQUENCE 243 AA; 28067 MW; 12817823 CRC32;

Query Match Score 429; DB 1; Length 243;

Best Local Similarity 60.0%; Pred. No. 7.28e-65;
 Matches 23; Mismatches 16; Indels 1; Gaps 1;

Db 24 VAPEPPKAPPAPAPPAPPLRRSSSANRYSTATEPKVKKPISASRKIQLNNTMMQLIQA
 K 83
 :|: ::|: ::|: ::|: ::|: ::|: ::|: ::|: ::|: ::|: ::|: ::|: ::|: ::|:
 :|: ::|: ::|: ::|: ::|: ::|: ::|: ::|: ::|: ::|: ::|: ::|: ::|: ::|:
 QY 1 MADGSSDAARPRPAPRPRPAPRPRSS-NTRAYATEPAKKKRSASRKQLKTLQLIQA
 K 59

Db 84 EMEREERERAREKERYLAERQPLQLGSRLSEREOLDCQE 123
 :|: ::|: ::|: ::|: ::|: ::|: ::|: ::|: ::|: ::|: ::|: ::|: ::|:
 QY 60 ELEREEAEERRGEKGRALSTRCOPLELAGLGFAELQDLCRQ 99

RESULT 8 STANDARD; PRT; 168 AA.
 ID TRIC_CHICK
 AC P27673;
 DT 01-AUG-1992 (REL. 23, CREATED)

DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)

DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)

DE TROPONIN I, CARDIAC MUSCLE (FRAGMENT).

OS GALLUS GALLUS (CHICKEN).

OC EURYCTOA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;

OC NEognathae; GALLIFORMES; PHASIANIDAE; PHASIANAE; GALLUS.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 92011768.

RA HASTINGS K.E., KOPPE R.I., MARMUR E., BADER D., SHIMADA Y.,

RA TOURA N.;

RT Structure and developmental expression of tropomodulin I isoforms. CDNA

CLONE ANALYSIS OF AVIAN CARDIAC TROPONIN I mRNA.";

J. BIOL. CHEM. 266:19659-19665(1991).

CC -!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE

THIN FILAMENT REGULATORY COMPLEX WHICH CONFERs CALCIUM-SENSITIVITY.

CC -!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.

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 CC or send an email to license@isb-sib.ch).

CC -!- DR EMBL; M73703; G212821;

DR PFAM; PF00992; Tropomodulin 1.

KW MUSCLE PROTEIN; ACTIN-BINDING.

"Cardiac tropomodulin I is a heart-specific marker in the Xenopus embryo:

RT

FT	NON_TER	1	1	OS HOMO SAPIENS (HUMAN).
SQ	SEQUENCE	168 AA;	18979 MW;	F25BBADF CRC32;
Query Match	Score 39.3%; Best Local Similarity 65.5%; Matches 37; Conservative	Score 268; Pred. No. 4; 7.1e-32;	DB 1; Length 168;	
Db	1 KIQKLTULLQRAKRELEREQERAGKHLGGCPPELEGVAQOLQELCRE 54	6; Mismatches 11; Indels 0; Gaps 0;		
Qy	46 KIQKLTULLQIAKELREAEERRGEKRALSTRCQPLLELAGLGFAELDLCRQ 99			
RESULT	9	STANDARD;	PRT;	186 AA.
ID	TRIS_RAT			
AC	P13413;			
DT	01-JAN-1990 (REL. 13, CREATED)			
DT	01-JAN-1990 (REL. 13, LAST ANNOTATION UPDATE)			
DT	01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)			
DE	TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM).			
DN	TNNII.			
OS	RATTUS NORVEGICUS (RAT), EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;			
OC	RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SEQUENCE-BLOOD;			
RX	MEDLINE: 94193765.			
RA	CORIN S.J., JUHASZ O., ZHU L., CONLEY P., KEDES L., WADE R.;			
RT	"Structure and expression of the human slow twitch skeletal muscle troponin I gene."			
RL	J. BIOL. CHEM. 269:10651-10659(1994).			
CC	-!- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERs CALCIUM-SENSITIVITY			
CC	TO STRIATED MUSCLE ACTOMYOSIN ATPase ACTIVITY.			
CC	-!- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.			
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CC	CC	CC	CC	CC
DR	J04760; G339965; -			
DR	EMBL: L21910; I437009;			
DR	EMBL: L21906; G437009; JOINED.			
DR	EMBL: L21908; G437009; JOINED.			
DR	EMBL: L21909; G437009; JOINED.			
DR	PIR: A35355; A35355.			
DR	MIM: 191042; -			
DR	PFAM: PF00992; Troponin; 1.			
DR	MUSCLE PROTEIN ACTIN-BINDING.			
FT	INIT MET 0 0			
FT	DOMAIN 1 47 INVOLVED IN BINDING TNC AND ACTIN.			
FT	CONFFLICT 181 182 KS -> NA (IN REF. 1).			
SQ	SEQUENCE 186 AA; 61561 MW; 6DABD050 CRC32;			
Query Match	Score 33.9%; Score 231; DB 1; Length 186;			
Best Local Similarity 50.7%; Matches 34; Conservative 14; Mismatches 19; Indels 0; Gaps 0;				
Db	1 PEVERKPKITASRKLLKSLMLAKAKEKCWEQEHEERAEKVYLAERIPPLQTGTLISLA 60			
Qy	33 PHAKKKSKISASRKQLQTKLQQAKQELEREAKERGEKRALSTRCQPLLELAGLGFAE 92			
RESULT	11	STANDARD;	PRT;	184 AA.
ID	TRIS_RABIT			
AC	P0245;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)			
DE	TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM).			
GN	TNNII.			
OS	ORYCTOLAGUS CUNICULUS (RABBIT), EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;			
OC	LAGOMORPHA; LEPODIDAE; ORYCTOLAGUS.			
RN	[1]			
RP	SEQUENCE: 78060392.			
RX	MEDLINE: 78060392.			

RESULT	12	TRIF_RABBIT	STANDARD;	PRT;	181 AA.
P02643;		21-JUL-1986	(REL. 01, CREATED)		
O1-JUL-1993		01-JUL-1993	(REL. 26, LAST SEQUENCE UPDATE)		
15-DEC-1998		15-DEC-1998	(REL. 37, LAST ANNOTATION UPDATE)		
TROPONIN I,		TROPONIN I,	FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM).		
TNNI2.					
ORYCTOLAGUS CUNICULUS (RABBIT)					
EUKARYOTA; METAZOA; CHORDATA; MAMMALIA; EUTHERIA;					
LAGOMORPHA; LEPODIAE; ORYCTOLAGUS.					
[1]		SEQUENCE FROM N.A.			
MEDLINE;	93094259.				
SHENG Z., PAN B. S., MILLER T., POTTER J.D.;					
"Isolation, expression, and mutation of a rabbit skeletal muscle cDNA clone for troponin I. The role of the NH2 terminus of fast skeletal muscle troponin I in its biological activity.",					
J. BIOL. CHEM. 267:25407-25413(1992).					
[2]		SEQUENCE FROM N.A.			
TISSUE-MUSCLE;					
MEDLINE;	93227244.				
WU Q.L., RAYCHODHURY M.K., DU Y., JHA P.K., LEAVIS P.C., SARKAR S.;					
Characterization of a rabbit fast skeletal troponin I cDNA: a comparative sequence analysis of vertebrate troponin I isoforms and tissue-specific expression of a single copy gene.					

[3] SEQUENCE FROM N. A.
MEDLINE; 93265949.
KLUWE L., MAEDA K., MAEDA Y.;
"E. coli" expression and characterization of a mutant tropomodulin I with
the three cysteine residues substituted.;
FEBS LETT. 323:33-88(1993).
[4] SEQUENCE.
MEDLINE; 76039510.
WILKINSON J.M., GRAND R.J.A.;
"The amino acid sequence of tropomodulin I from rabbit skeletal muscle.";

[5] REVISION. MEDLINE: 78111026

WILKINSON J.M., GRAND R.J.A.; "Comparison of amino acid sequence of troponin I from different striated muscles."; NATURE 271:31-35(1978).

[6] RN RN SEQUENCE OF 1-24 AND 165-177 FROM N.A. MEDLINE: 83167564.

RXN PUTNEY S.D., HERLIHY W.C., SCHIMMEL P.R.; "A new troponin T and cDNA clones for 13 different muscle proteins, found by shotgun sequencing"; NATURE 302:718-721(1983).

[7] RN RN RP PHOSPHORYLATION SITES. MEDLINE: 74309023.

RXN NOIR A.J.G., WILKINSON J.M., PERRY S.V.; "The phosphorylation sites of troponin I from white skeletal muscle of the rabbit"; FEBS LETT. 42:253-256(1974).

[8] RN RN RP PHOSPHORYLATION SITES. MEDLINE: 74308154.

RXN HUANG T.S., BYUND D.B., STULL J.T., KREBS E.G.; "The amino acid sequences of the phosphorylated sites in troponin I from rabbit skeletal muscle"; FEBS LETT. 42:249-252(1974).

[9] RN RN RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-47 IN COMPLEX WITH TNC. MEDLINE: 98226730.

RXN VASSILIEV D.G., TAKEDA S., WAKATSUKI S., MAEDA K., MAEDA Y.; "Crystal structure of troponin C in complex with troponin I fragment at 2.3 resolution"; PROC. NATL. ACAD. SCI. U.S.A. 95:4847-4852(1998).

RUL -1- FUNCTION: TROPONIN I IS THE INHIBITORY SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERNS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMIOSIN ATPASE ACTIVITY.

CC -1- TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.

CC CC DR DR EMBL: 104347; G165778; -.

CC CC DR DR EMBL: X14190; G506473; -.

CC CC DR DR EMBL: S61403; G409099; -.

CC CC DR DR EMBL: V00897; G1737; -.

CC CC DR DR EMBL: V00898; G929767; -.

CC CC PIR: A03087; TTBIS.

CC CC DR DR PDB: 1AZX; 15-JUL-98.

CC CC DR DR PFAM: PF00932; Troponin I.

CC CC KW KW MUSCLE PROTEIN; ACETYLATION; PHOSPHORYLATION; ACTIN-BINDING; 3D-STRUCTURE.

CC CC INIT_MET 0 0 ACETYLATION.

CC CC MOD_RIS 1 1 PHOSPHORYLATION (BY PKH).

CC CC MOD_RIS 11 11 PHOSPHORYLATION (BY CAPK).

CC CC MOD_RIS 117 117 INVOLVED IN BINDING TNC.

CC DOMAIN 1 47 INVOLVED IN BINDING TNC AND ACTIN.

CC DOMAIN 96 116 MISSING (IN REF. 4 AND 5).

CC DOMAIN 153 155 CONFLICT 191 21002 MED. 00230052 C222.

Query	Match	30.5%	Score 208;	DB 1;	Length 181;
Best Local Matches	Similarity 42.9%;	Pred. No. 1.60-20;			
Matches 27;	Conservative 19;	Mismatches 16;	Indels 1;	Gaps 1;	
Db	5 KRNRAITARRHLKSYMMLQIAATELEKEGRREASKQNYLAEHCPLSLPG-SMAEVQEL 63				
Qy	37 KKSKISASRKQLQKTLILQTAQOELERAAERRGEKKA 96				

INIT_MET 0 0 BY SIMILARITY.
FT DOMAIN 1 47 INVOLVED IN BINDING TNC.
FT DOMAIN 96 116 INVOLVED IN BINDING TNC AND ACTIN.
SQ SEQUENCE 181 AA; 21207 MW; 83ED65E4 CRC32;

Query Match 29.5%; Score 201; DB 1; Length 181;
Best Local Similarity 39.7%; Pred. No. 3.22e-19;
Matches 25; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

Db 5 KRNRAITAROHLKSYMQLQIAATELEKEESRREA
KONYLAENHCPLHIFPG-SMSEYQEL 63
|::: ::| :|:::||| |:::| |:::| |:::| |:::| |:::|
37 KRISKISASRKQLQLKTULLQIAQELREAEEERGERGRALSTRCOPLELAGLGFAELQDL 96
Db 64 CRQ 66
|:|
Qy 97 CRQ 99

Search completed: Fri Jan 21 14:28:03 2000
Job time : 20 secs.